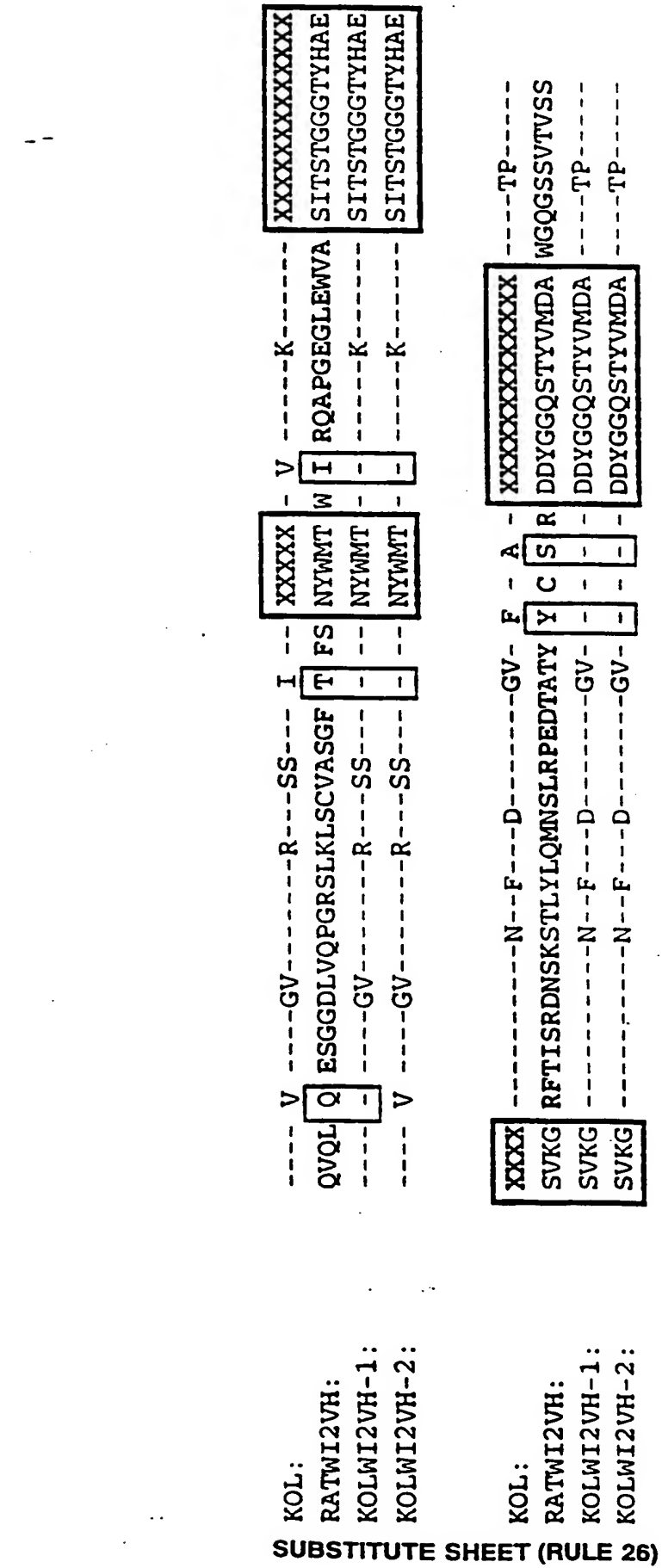
KOL: ---- V ----GV-------R---SS--- I --- XXXXX - V -----K------ XXXXXXXXXXXX
RATWI2VH: QVQL Q ESGGDLVQPGRSLKLSCVASGF T FS NYWMT W I RQAPGEGLEWVA SITSTGGGTYHAE
KOLWI2VH-1: ---- - ----GV-------R---SS--- - -- NYWMT - - -----K------ SITSTGGGTYHAE
KOLWI2VH-2: ---- V ----GV-------R---SS--- - -- NYWMT - - -----K------ SITSTGGGTYHAE
KOL: XXXX ----------N--F---D-------GV- F - A - XXXXXXXXXXXX ----TP-----
RATWI2VH: SVKG RFTISRDNSKSTLYLQMNSLRPEDTATY Y C S R DDYGGQSTYVMDA WGQGSSVTVSS
KOLWI2VH-1: SVKG ----------N--F---D-------GV- - - - - DDYGGQSTYVMDA ----TP-----
KOLWI2VH-2: SVKG ----------N--F---D-------GV- - - - - DDYGGQSTYVMDA ----TP-----

FIG. 1

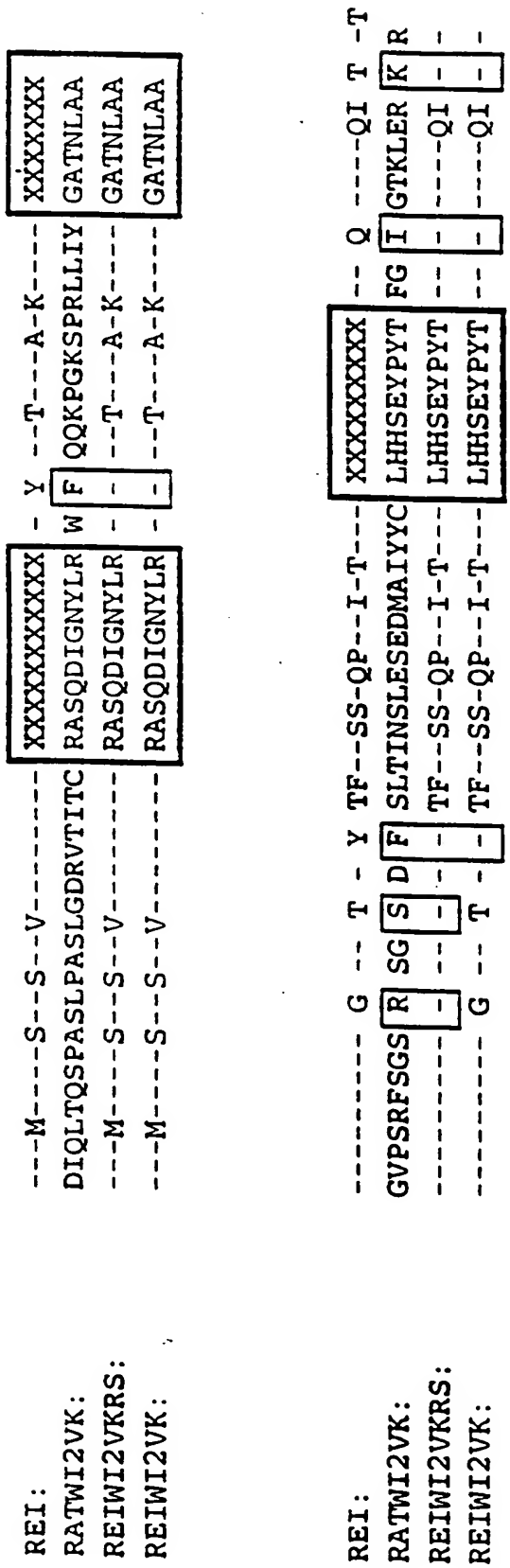
REI: ---M----S--S--V-------- XXXXXXXXXXX - Y --T---A-K---- XXXXXXX
RATWI2VK: DIQLTQSPASLPASLGDRVTITC RASQDIGNYLR W F QQKPGKSPRLLIY GATNLAA
REIWI2VKRS: ---M----S--S--V-------- RASQDIGNYLR - - --T---A-K---- GATNLAA
REIWI2VK: ---M----S--S--V-------- RASQDIGNYLR - - --T---A-K---- GATNLAA
REI: --------- G -- T - Y TF--SS-QP--I-T--- XXXXXXXXX -- Q ----QI T -T
RATWI2VK: GVPSRFSGS R SG S D F SLTINSLESEDMAIYYC LHHSEYPYT FG I GTKLER K R
REIWI2VKRS: --------- - -- - - TF--SS-QP--I-T--- LHHSEYPYT -- - ----QI - -
REIWI2VK: --------- G -- T - - TF--SS-QP--I-T--- LHHSEYPYT -- - ----QI - -

FIG.2

FIG.3A

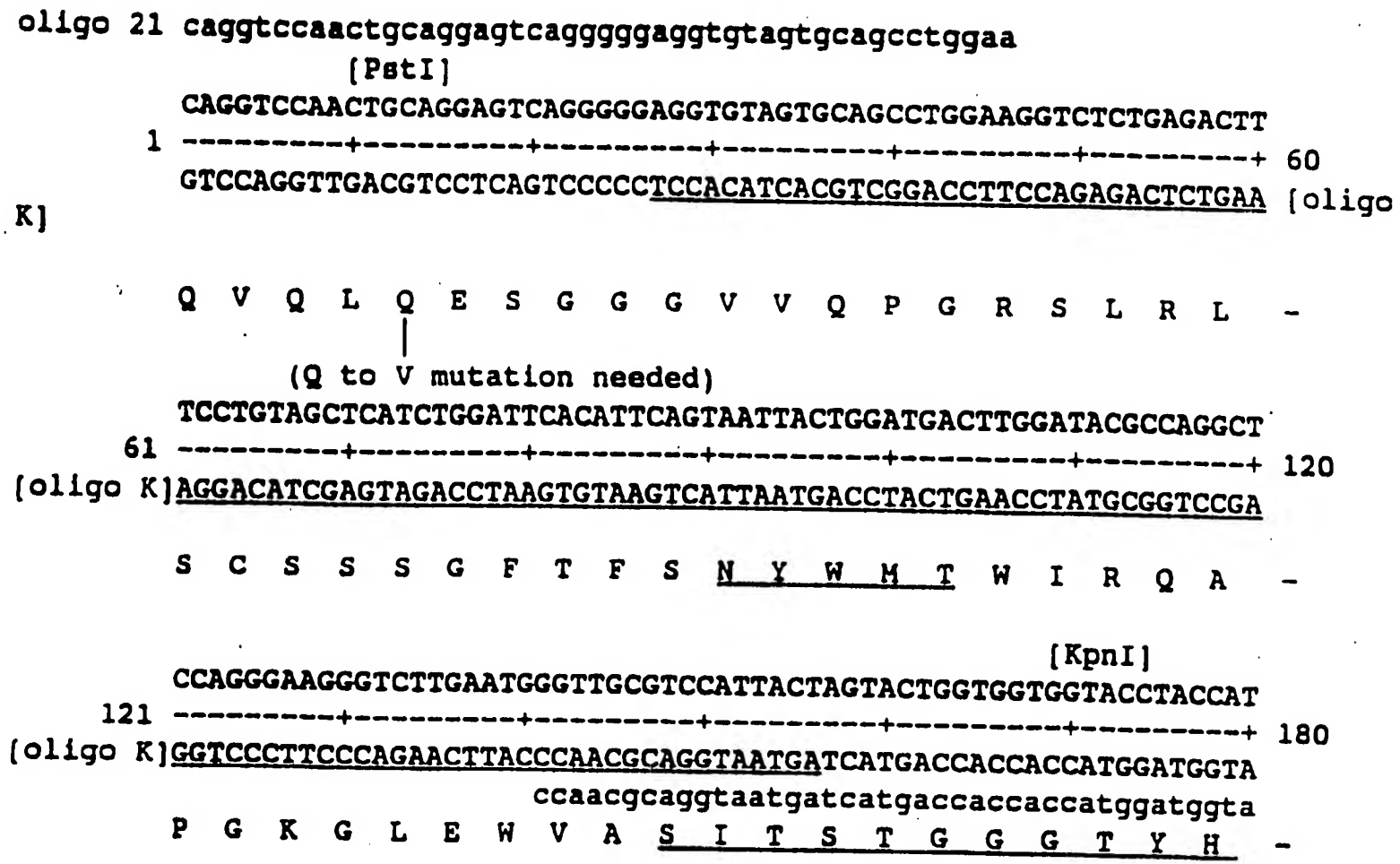

FIG.3B

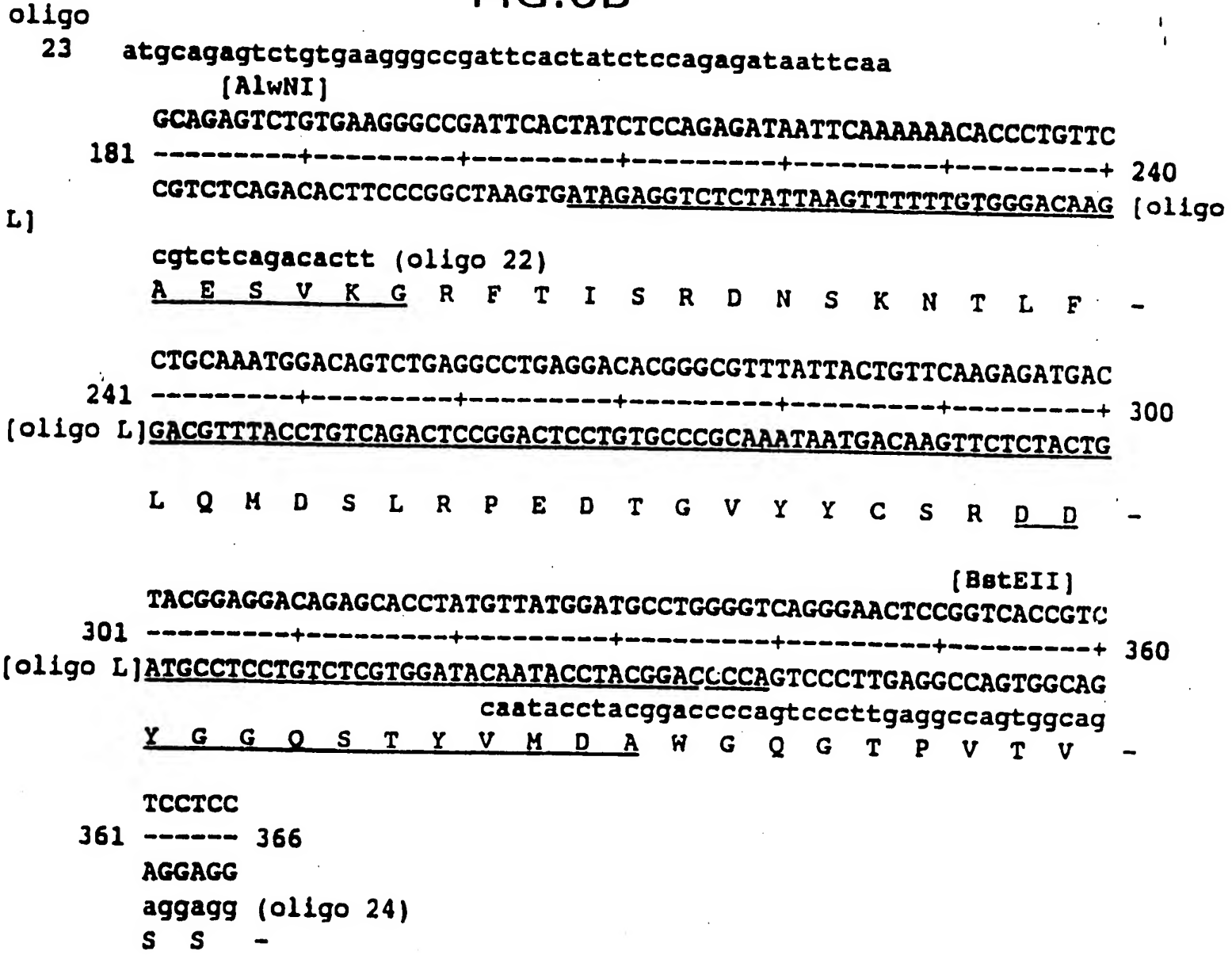

FIG.4A

```
oligo 25 (PvuII)
         gacattcagctgacccagtctccatcttccctgtctgcgtctgtgggaga
oligo 25          atgacccagtctccatcttccctgtctgcgtctgtgggaga
         GACATTCAGATGACCCAGTCTCCATCTTCCCTGTCTGCGTCTGTGGGAGACAGAGTCACT
       1 ---------+---------+---------+---------+---------+---------+ 60
         CTGTAAGTCTACTGGGTCAGAGGTAGAAGGGACAGACGCAGACACCCTCTGTCTCAGTGA (oligo
M)

         D  I  Q  M  T  Q  S  P  S  S  L  S  A  S  V  G  D  R  V  T  -

         ATTACTTGCCCGGGCAAGTCAAGACATTGGAAATTATTTAAGATGGTTCCAGCAGACACCG
      61 ---------+---------+---------+---------+---------+---------+ 120
(oligo M)TAATGAACGGCCCGTTCAGTTCTGTAACCTTTAATAAATTCTACCAAGGTCGTCTGTGGC

         I  T  C  R  A  S  Q  D  I  G  N  Y  L  R  W  F  Q  Q  T  P  -

                                              oligo 27  tggctgcaggggtcccatca
                                                          [PstI]
         GGGAAAGCTCCGAAACTTTGATTTATGGTGCAACCAACTTGGCTGCAGGGGTCCCATCA
     121 ---------+---------+---------+---------+---------+---------+ 180
(oligo M)CCCTTTCGAGGCTTTGAAAACTAAATACCACGTTGGTTGAACCGACGTCCCCAGGGTAGT
                                actaaataccacgttggttgaaccgacgtccccagg (oligo 26)
         G  K  A  P  K  L  L  I  Y  G  A  T  N  L  A  A  G  V  P  S  -
```

FIG.4B

```
                cggttcagtggcagtgggtctggg
                CGGTTCAGTGGCAGTGGGTCTGGGACAGATTTTACTTTTACCATCTCAAGCCTTCAGCCT
          181 ----------+----------+----------+----------+----------+----------+ 240
[oligo N] GCCAAGTCACCGTCACCCAGACCCTGTCTAAAATGAAAATGGTAGAGTTCGGAAGTCGGA

                R  F  S  G  S  G  S  G  T  D  F  T  F  T  I  S  S  L  Q  P  -

                GAAGATATTGCTACTTATTACTGTCTGCACCATTCTGAGTATCCATACACGTTTGGAATT
          241 ----------+----------+----------+----------+----------+----------+ 300
[oligo N] CTTCTATAACGATGAATAATGACAGACGTGGTAAGACTCATAGGTATGTGCAAACCTTAA
                                                tgtgcaaaccttaa
                E  D  I  A  T  Y  Y  C  L  H  H  S  E  Y  P  Y  T  F  G  I  -

                GGGACCAAGTTGCAGATCAAACGTG
          301 ----------+----------+----- 325
[oligo N] CCCTGGTTCAACGTCTAGTTTGCAC
                cctggttcaacgtctagattgcac (oligo 28)

                G  T  K  L  Q  I  K  R  -
```

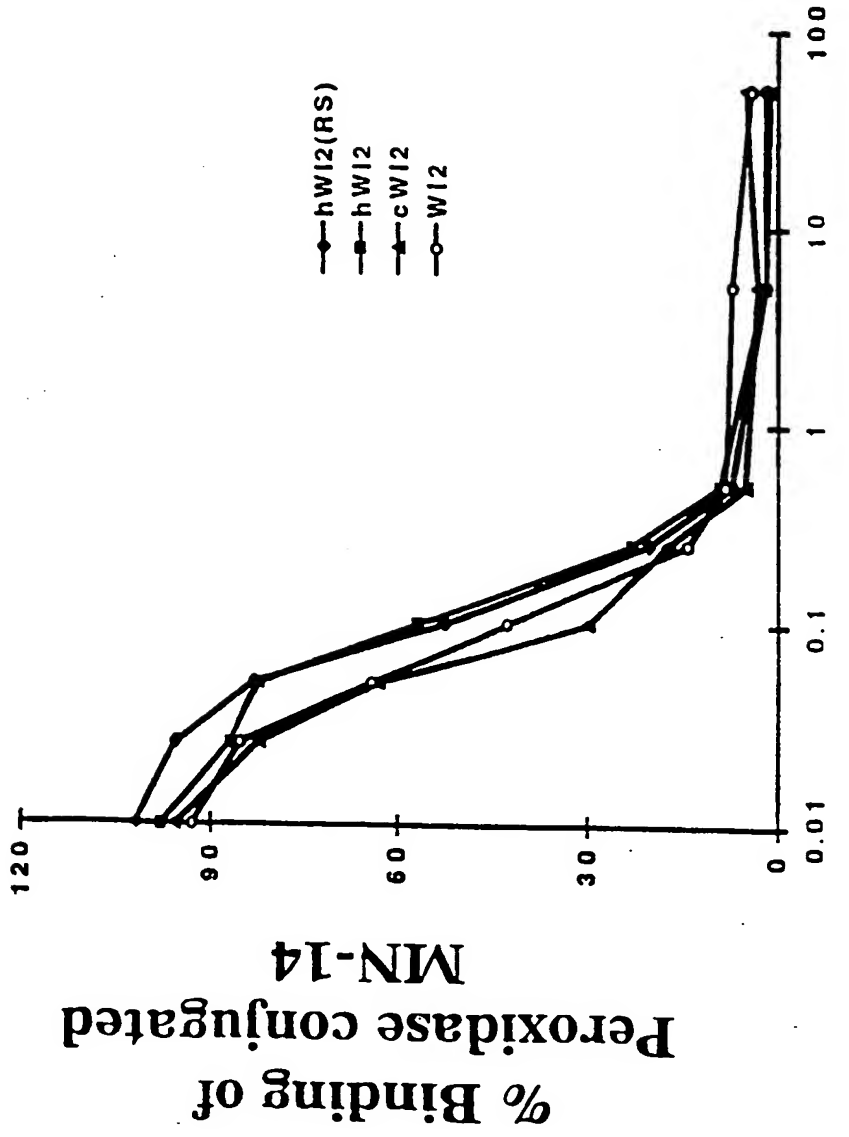
% Binding of Peroxidase conjugated MN-14
120
90
60
30
0
0.01
0.1
1
10
100
Concentration of competing antibodies (µg/ml)
hWI2(RS)
hWI2
cWI2
WI2

FIG.5

```
GACATTCAGC TGACCCAGTC TCCAGCTTCC CTGCCTGCGT CTCTGGGAGA
CTGTAAGTCG ACTGGGTCAG AGGTCGAAGG GACGGACGCA GAGACCCTCT
D  I  Q  L    T  Q  S    P  A  S    L  P  A  S    L  G  D
                                                              50

CAGAGTCACT ATTACTTGCC GGGCAAGTCA AGACATTGGA AATTATTTAA
GTCTCAGTGA TAATGAACGG CCCGTTCAGT TCTGTAACCT TTAATAAATT
 R  V  T    I  T  C  R  A  S  Q  D  I  G  N  Y  L  R
                      CDR1
                                                             100

GATGGTTCCA GCAGAAACCG GGGAAATCTC CGAGGCTTTT GATTTATGGT
CTACCAAGGT CGTCTTTGGC CCCTTTAGAG GCTCCGAAAA CTAAATACCA
  W  F  Q    Q  K  P    G  K  S  P    R  L  L    I  Y  G
                                                             150

GCAACCAACT TGGCAGCTGG GGTCCCATCA CGGTTCAGTC GCAGTAGGTC
CGTTGGTTGA ACCGTCGACC CCAGGGTAGT GCCAAGTCAC CGTCATCCAG
A  T  N  L    A  A  G    V  P  S    R  F  S  G    S  R  S
   CDR2
                                                             200

TGGGTCAGAT TTTTCTCTGA CCATCAACAG CCTGGAGTCT GAAGATATGG
ACCCAGTCTA AAAAGAGACT GGTAGTTGTC GGACCTCAGA CTTCTATACC
 G  S  D    F  S  L  T    I  N  S    L  E  S    E  D  M  A
                                                             250

CTATTTATTA CTGTCTGCAC CATTCTGAGT ATCCATACAC GTTTGGAATT
GATAAATAAT GACAGACGTG GTAAGACTCA TAGGTATGTC CAAACCTTAA
  I  Y  Y    C  L  H    H  S  E  Y    P  Y  T    F  G  I
                      CDR3
                                                             300

GGGACCAAGC TGGAACGGAA ACGG
CCCTGGTTCG ACCTTGCCTT TGCC
G  T  K  L    E  R  K    R
                                                             324
```

FIG.6

```
CAGGTCCAAC TGCAGGAGTC AGGGGGAGAT CTAGTGCAGC CTGGAAGGTC          50
GTCCAGGTTG ACGTCCTCAG TCCCCCTCTA GATCACGTCG GACCTTCCAG
Q  V  Q  L   Q  E  S   G  G  D   L  V  Q  P   G  R  S

TCTGAAACTT TCCTGTGTAG CCTCTGGATT CACATTCAGT AATTACTGGA          100
AGACTTTGAA AGGACACATC GGAGACCTAA GTGTAAGTCA TTAATGACCT
 L  K  L   S  C  V  A   S  G  F   T  F  S   N  Y  W  M
                                              CDR1

TGACTTGGAT CCGCCAGGCT CCAGGGGAGG GTCTTGAATG GGTTGCGTCC          150
ACTGAACCTA GGCGGTCCGA GGTCCCCTCC CAGAACTTAC CCAACGCAGG
 T  W  I   R  Q  A   P  G  E  G   L  E  W   V  A  S

ATTACTAGTA CTGGTGGTGG GACTTACCAT GCAGAGTCTG TGAAGGGCCG          200
TAATGATCAT GACCACCACC CTGAATGGTA CGTCTCAGAC ACTTCCCGGC
I  T  S  T   G  G  G   T  Y  H   A  E  S  V   K  G  R
                    CDR2

ATTCACTATC TCCAGAGATA ATTCAAAAAG CACCCTGTAC CTGCAAATGA          250
TAAGTGATAG AGGTCTCTAT TAAGTTTTTC GTGGGACATG GACGTTTACT
 F  T  I   S  R  D  N   S  K  S   T  L  Y   L  Q  M  N

ACAGTCTGAG GCCTGAGGAC ACGGCCACTT ATTACTGTTC AAGAGATAGAC         300
TGTCAGACTC CGGACTCCTG TGCCGGTGAA TAATGACAAG TTCTCTATCTG
  S  L  R   P  E  D   T  A  T  Y   Y  C  S   R  D  D

TACGGAGGAC AGAGCACCTA TGTTATGGAT GCCTGGGGTC AGGGATCTTC          350
ATGCCTCCTG TCTCGTGGAT ACAATACCTA CGGACCCCAG TCCCTAGAAG
Y  G  G  Q   S  T  Y   V  M  D   A  W  G  Q   G  S  S
                    CDR3

GGTCACCGTC TCCTCA                                               376
CCAGTGGCAG AGGAGT
 V  T  V   S  S
```

FIG.7